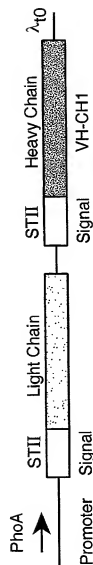


Fab Expression Vector pAK19



Full Length Antibody Expression Vector Derived from pAK19

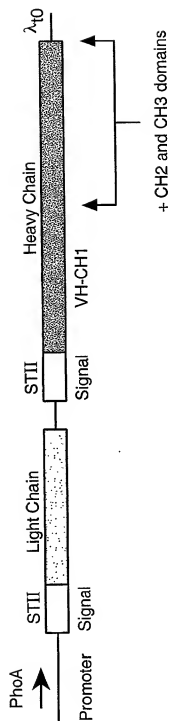


FIG. 1

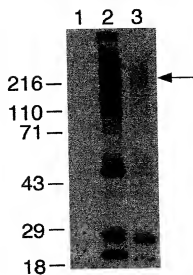
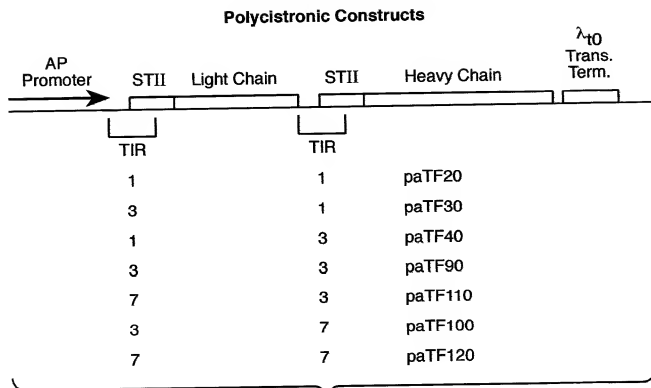
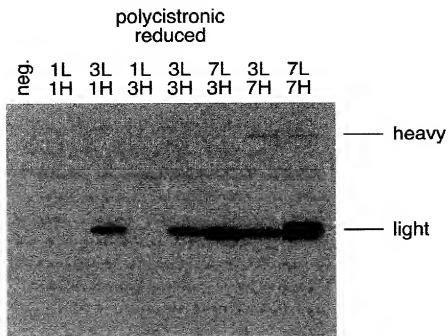
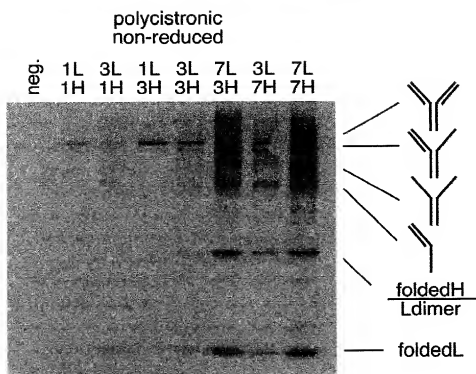
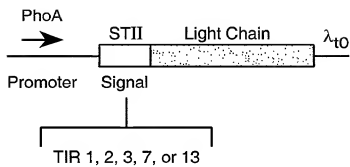
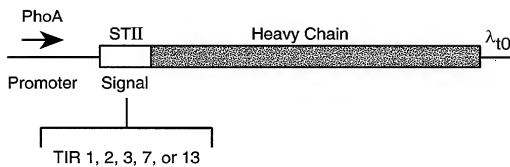
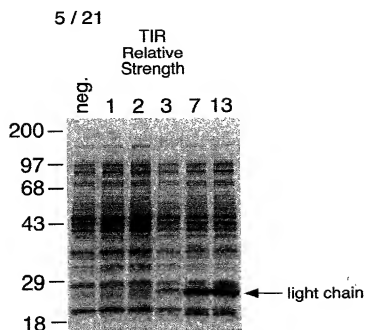
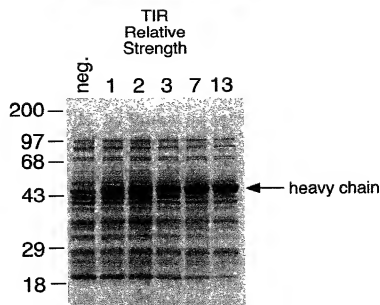
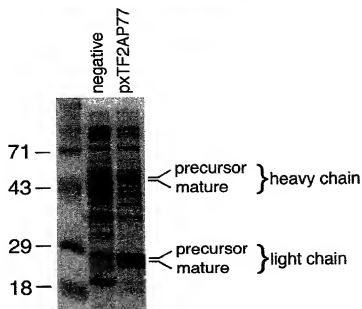
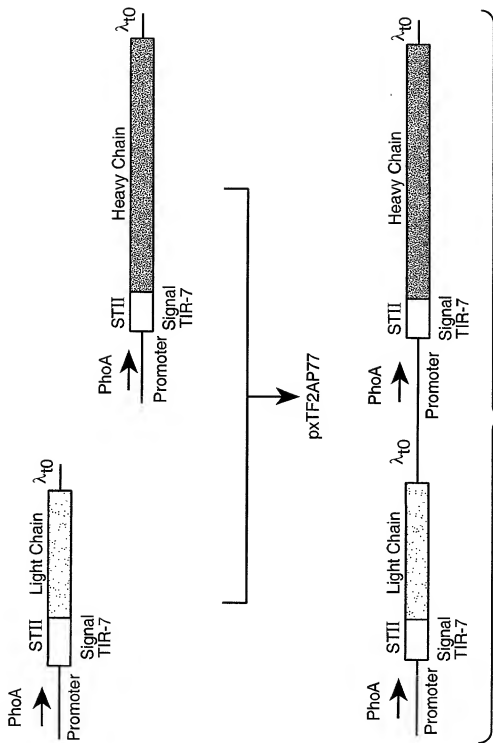
**FIG._2****FIG._3**

FIG._4A**FIG._4B**

Light Chain Constructions**Heavy Chain Constructions****FIG. 5**

**FIG._6A****FIG._6B****FIG._8**



Separate Cistron Constructs

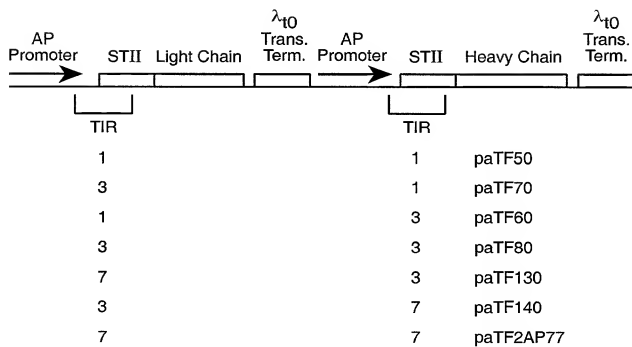
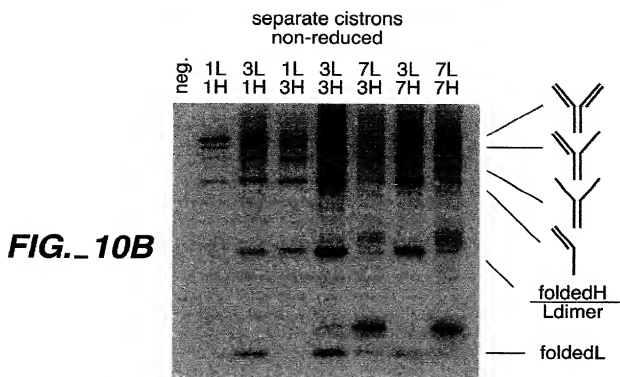
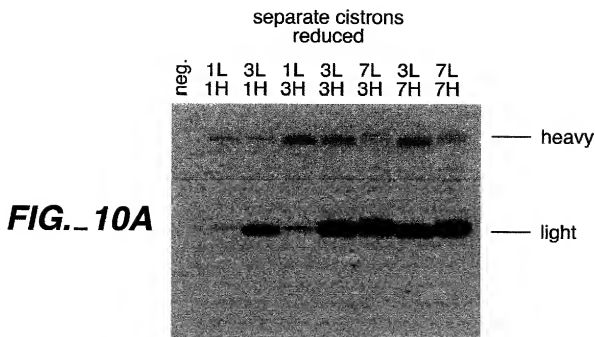
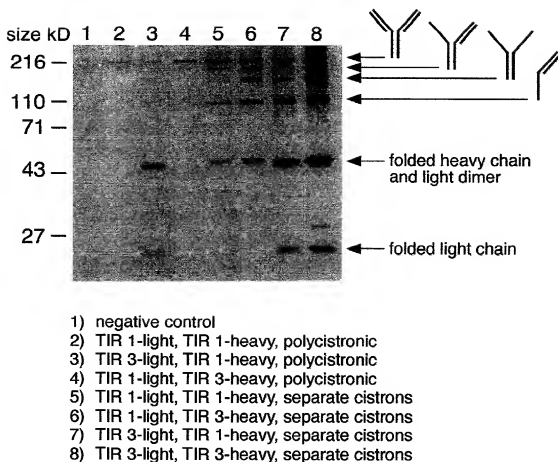
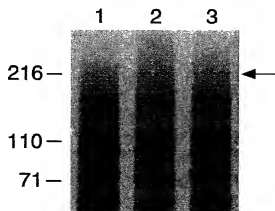


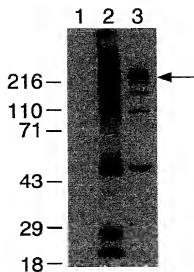
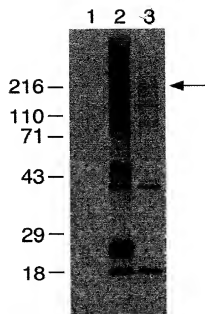
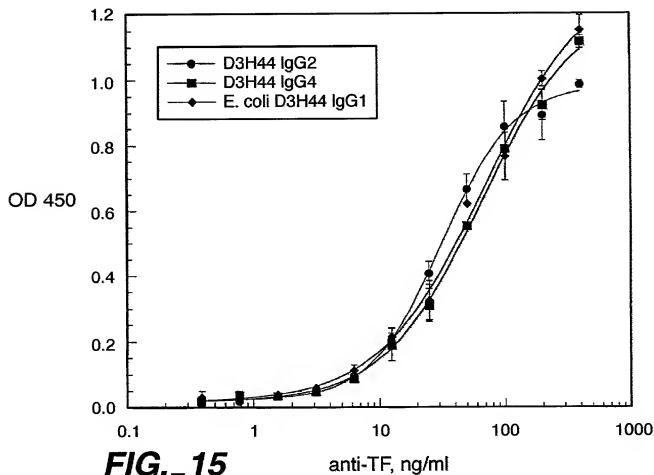
FIG. 9



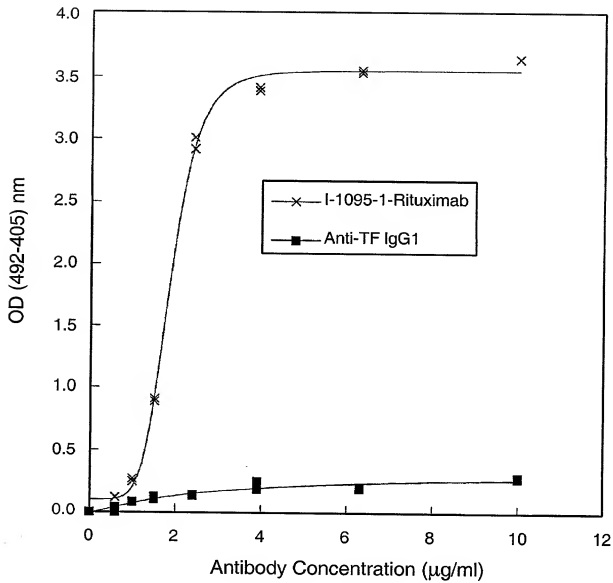
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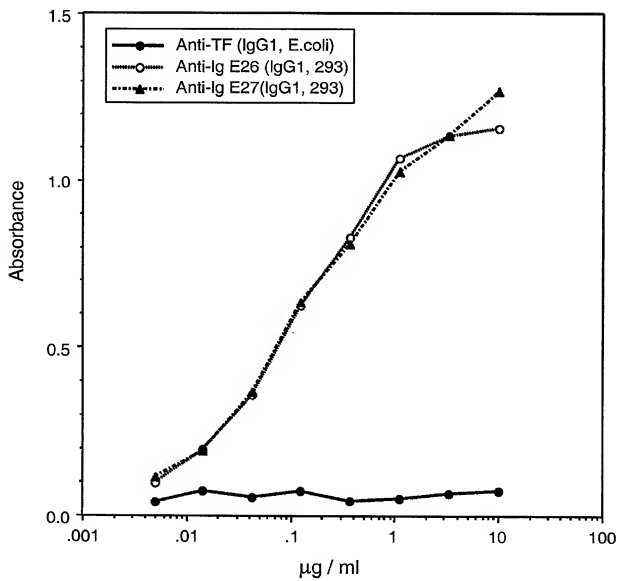
**FIG. 11****FIG. 12**

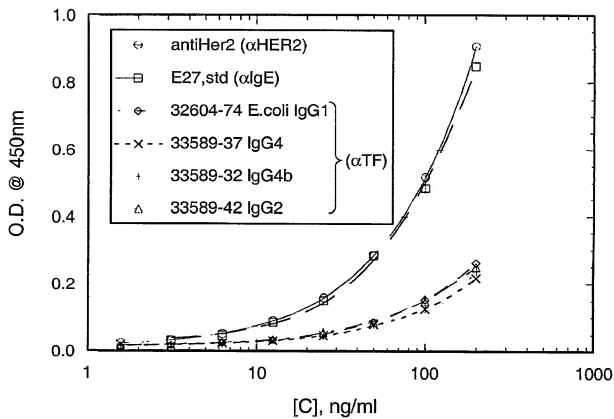
10/21

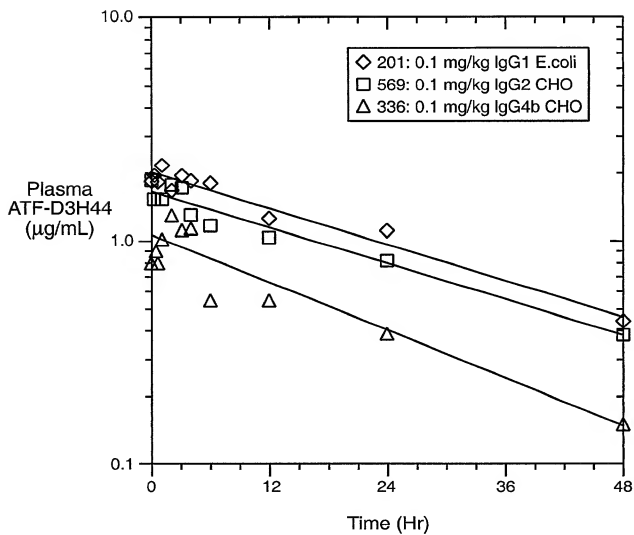
**FIG. 13****FIG. 14****FIG. 15**

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**FIG._16**

**FIG. 17**

**FIG._18**

**FIG._19**

1 GRANTCACT TCTCCATCT TGGATAGG AATACAGAC ATGAAATTC TCAATGCTGA GTGTATATT AAGCTTGCC AAAAAGAAGA AGAGTCAGT
CTTAAGTGA AGAGTATGA AACCTATTC TTATATCTG TACTTTTAG ATTAAGACT CACCAATAA TTGAAAGCG TTTTCTCTCT TCTCAGTTA
101 GAAGTCTG OCAGAGTAG AGCTTTGAG ATTATGCTA CTGCAATGCT TGCATATGTC TGCATATGTC ACCACAGCG GTTGAATGAT CAGGTAGAG
CTTGACAC GGTTCATCT TCGAACTC TAAATAGAGT GAGCTTAGA AGCTTTAGC CCGTTTTC TGGTCTGCG CAACTAATA GTTCACTTC
201 GGCCCTGTA CAGGTATGA CCGATGCTA GAGCTATAG CAGCTATAG GAGCTGTCG CCGATTAAT AAAGAGTTA TTGAAGCATC CTGTGCTAT
CCCGAGAT CTTCATCT CAGTATAGT CAGTATAGT CAGTATAGT CAGTATAGT CAGTATAGT CAGTATAGT CAGTATAGT CAGTATAGT
301 AAAAGTAT CTCTTACA CTGTCTATA GCTGTACAG GCGAGACT ATAGTGTCTT TCTTTTAT TTATATGA TTGTATGA GTAGCGAGT
TTTTCAATA GAAGTATG CAGAGTAT TCACAGTTC CCGCTTGA TATCAGCGA ACAAATTA AAAATATAT AACATATGAT CAGTCTTCA
401 TCACTAAAA AGGTATCTA GAATATGAA GAAGATATC GAATATCTA CTATCTTTC TTGATCTTTC GTTGTCTTTC TCTATGCTA CAAAGCGATA CCGTATATC
AGTGCATTTT TCCATATGAT CTATATATCT CTCTCTATG CATTATAGAG AAGCTATGATA CAAAGAAA AGATATAGT GTTTCAGAT CCGTATATC
1 M K K N I A F L L A S M F V F S I A T N A Y A D I
Anti-tissue Factor Light Chain*

*STII Signal Sequence TIR-1

501 CAGATCAAC AGTCCGAG CTCCCTGTC GCTCTGTC GCGATAGGT CACATACCC TCCAGACCA GTGCGACAT CAGAGCAT CTGACTGTG
GTCTACTGG TCAAGGCTC GAGGACAG GCGAGACCC CCGTATCCA GTGTATGTC AGCTTGGT CAGCGTGA GTTCTGATA GACTTGA
26 Q M T Q S P S L S A S V G D R V T I T C R A S R D I K S Y L N W Y
601 ATCAGAGA ACCAGAAA GCTCCAGG TACTATATTA CTATCTACT AGTCTGTC AGAGTATCC TTCTGCTTC TTCTGATCC GTTCTGAGC
TAGTATCTT TGTCTCTTT CAGGCTTTC ATGATTAAT GATACATCA TCAAGCAGC TTCTCAGAG AAGCGAG AGCTATAGC CAGAGCTTC
60 Q Q K P G K A P K V L I Y A T S L A E G V P S R F S G S G S G T
701 GATATCACT CAGACATCA CAGTCTGCA CCGAGAGC TTCCACTT ATTTCTCT TCAAGAGA GAGTCTCAT GAGATATG CAGAGTATC
CTATATGGA GAGTGTAGT GTTCAAGAT CAGTCTGTC AGCTTATGA TATATAGGA AGTGTCTT CTAGAGTA CTTGTATAC CTGTATAC
93 D Y T L T I S L Q P E D F A T Y I C L Q H G E S P W T F G Q G T
801 AGGTGAGA TCAAGAC TGTGCTGCA CAGTCTCT CAGTCTCT TCACTTCC GCGATATC GAGCTATGA AATCTGAC TGTCTCTCT GTTGTCTTC
TTCCACTT AGTCTGTC ACTGAGAT CAGAGAGT GAGAGAGA AGTATAGG CAGTATCA CTGTCTAT TTAGCTTC ACGAGACA CAGAGCTTC
126 K V E I K R T V A P S V F I P P S D E Q L K S G T A S V V C L L
901 TGAATATCT CTATCCAGA GAGGCCAAG TACATGGA GGTGATTA GCGTCTCAT CCGTATCT CCGAGAGT GTACAGAGC AGAGCTAGC
ACTATATGA GATGAGTCT CTGCTGTC ATGCTATCT CAGCTATG CAGCTATG GCGATATG GCGTCTCA GAGTCTTC CAGTCTTC TCTGTCTT
160 N N F Y P R E A K V Q W K Y D N A L Q S G N S Q E S V T E Q D S K
1001 GAGAGTCC TACAGCTCA CAGAGCTCT GAGCTGAG CAGTATGAG AAGCTATCT ACGAGACA CAGATCTAC CCGTCCAGC TCAACCTCA GCGCTGAGC
CTGTGCTG ATGATGAT GTCTGTGGA CTGAGATCT TTCTCTCA TCTCTTCT CAGTCTG CAGAGCTTC AGTGTGAT CCGAGCTTC CCGAGCTTC
193 D S Y T S L S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCTCA CAAAGACT CAAAGAGGGA GAGTATAT TAAATCTT ACCTGCTGAG CTATGTGCG AGTGTGTC CCGGAGTCT AGGCTATAG
AGCGGCTG GTTCTGAA GTTGTCTCT CTACATATTA ATTATAGGA TCGGCTTC TCGGCTTC TCGGCTTC TCGGCTTC
226 S P V T K S F N R G E C O

FIG.-20a

1201 CTGGTGTGCG GCGGGGGT TTTTATGTT GCGAGGCGC ATCTGCAATG AACGTGTGCG TTATGTGAGA GCTTTGGAGA TTATGTGAC TGCATGCTTT
 GAGCCACGCG GCGCCCGGAA AAAATACAA CAGCTGCGCG AGCTGCTTAC TACGTACACG CGTCTCACTTT CAAAACCTCT AATPACAGTG AGGTACGAGA
 1301 GCGAATATGG CCGAAATAGA CCACACAGCG TGTATGATGC AGGTACGAGG GCGCTCTTAC GAGGTAAAGC CCGATGCGAG CATCTCTGAC GACCAATACG
 GCGTTATACG GCGTTTACT GGTGTGTGCG ACCTACTGAG TCCHTCTCC CCGCGACATG CTCACATTGG GACTATGGTC GTTAGGACTG CTGTCTATGC
 1401 AGCTCTGCGC CCGATATGTA AGAGAGTATF TGAACATCC TCGTCACTGA AAAAGTATATC TTATTCACAG CAGCATATAA GTTGTACAGG CCGAGACTTA
 TCGACGCGCC GCTATATGCAT TTTCTCATAT TCTGTCTTAG ACCAGTATTC TTTCATATGAC AAAGTATGTC GACATATATT CACAGATGTC CCGCTTGAT
 1501 TAGTCTGCTT GCTTTTATTT TTTTATGATF TTTGTACTGAG TACCAAGATT CAGGTAAAAA GGGTATCTAG AATATATGAG AAGATATGCT CATCTCTCT
 ATACAGGAAA CAAAAATAAA AATATACATA AACTGTGATC AAGGTGTCAA GTGCATTTT CCGATGATC TTATPACTAT TTTCTTATGAG GTTAGGACG GTTAGGAGA
 1601 TGCATCTGAG TTGCTTTTIT CATTGCTTAC AATCCGCTAC GCTGAGGATC AGCTGTGAGA GTCTGGCGGT GCTCTGGTGC AGCCAGGGGG CTTACTCTGT
 ACGTATGATC AAGCAAAAAA GATPACAGTG TTTGCGGCTG GACTTCAGAG TCGACCACTT CAGACCGCAA CCGGACCAAG TCGTCTCCCG GAGTAGGCGA
 10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
 *Anti-Tissue Factor Heavy Chain
 1701 TTGTCCTGAG CAGCTTCTCG CTTCAATATT AAGGAGTACT ACATGCTACT GGTTCGCTCAG GCGCGCGGTA AGGCGCTGGA AUGGCTTGA TTGATGATC
 AACAGGACAC GTGAGAGAC TTCTCTATGA TTGTAGTATC CAGAGGCTGTC CCGGCGCGCTT TCGCGGACT TCGCGCACTT TACCCACTT AACTACTGAG
 43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P
 1801 CAGCAGCAGG CAACACGATC TATGACCGGA AGTTCGAGA CCGTGCCTACT ATTAGCGCTG ACATTCGAA AAMCAGCA TACTGCGAGA TGAACAGCT
 GTCTCTGTC CTTGTGCTAG ATACTGCGCT TCAAGTCTCT GCGAGGTGTA TATTCGCGAC TGTAAAGGTT TTGTGTGCTT ATGAGGCTCT ACTTGTGGA
 77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L
 1901 GCGTGTGAG GACTGTGCG TCTATATATT TGTCTGACAG TCGCGTCTG ACAGTCTGTC AGCGGCGGTA TCGAGCTGAT GACCCAGTT CTTTGGGAC AGTGGCAGG GAGCGCGAG
 CCGACGACTC CTGTGACGCG AGATATATAC ACAGTCTGTC TCGCGCGGTA TCGAGCTGAT GACCCAGTT CTTTGGGAC AGTGGCAGG GAGCGCGAG
 110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S
 2001 ACCAGGGCG CATCGCTCTT CCGCTTGCCA AGAGCTGGA TCGCGGCGCA GCGCGCTGGS GCTGCTGCTT CAGGAGTAC TTCCCGCGAC
 TGCTTCCGG GTAGCGAGT P L A P S S K S T S G G T A A L G C L V K D Y F P E P
 143 T K G P S V F
 2101 CGGTACGCT GTGTGTGAC TCAGCGGCG TCACAGCGG TCGCGCTGCT TCTGCTGCTG CTAAGCTGAG CTAAGCTGAG TACTCTCTCA CCGAGTGTG
 GCGATGCGA CAGCACTCTG AGTCCGCGG ACTGTGCGC CCGCTGCTG AGGCGCGAC AGGCTGCTGAG GAGTCTGAG AGTGGGAGT CCGTGTGACCA
 177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V
 2201 GACTGTGCG TCTGACGCT TCGCGCGCA GACTTATATC TCGCATGCTA ATACAGCG CAGCAGCGC AAGGTGCGA AAGATGCTA GCGCAATCT
 CTGACGCGG AAGTGTGGA ACCGTGCTT CTGATGAG AGCTTGTCT TACTGCTGAG TTTCACTCT TCTTCTACT TCTTCTACT GCGCAATCT
 210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

FIG.-20b

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2301 TGTGACAAA CTCACATAC CCAACAGTTC CCAACAGTTC GGGACGCTCA GTCTCTCTCT TCTCCCCAAA ACCAAGGAC ACCCTCATGA
 243 CACATCTTTT GAGTGTGAT TATGAGGAC CTTCTGGAGT CAGAAGAGA AGGGGGTCTT TGGGTCTCTG TGGGAGTACT
 2401 TCTCTGCGGC CCGTCTAGTC ACTACGCTGG TGGTGGAGT GAGCCACGAA GACCTCTGAGG TCAAGTTCAA GTCCGTCAGTG GACGCGCTGG ATCGACTATA
 277 S R T P E V T C V V D V S H E D P E V K F N W Y V D G V E V H N
 2501 TGTCAAGACA AAGCGCGGG AGAGGACAGTA CACACACAG TACCGGTCTG TCAAGCTCTCT CACCGTCTCTG CACCCAGGACT GGCCTGATGG CAGAGGTAC
 310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y
 2601 AAGTGCACAGG TCTCCACAA AGCCTTCGCA GCGCCCATG AGAATACTAT CTCTCAAGCC AAGGGCAGC CCGCAGAAC ACCAGGTATC ACCCTGCCCC
 343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P F
 2701 CACCGCGGAC AACTCACGA CCAAGCCTCC CAGCTCTGAC TCAAGCTGAC CAGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q
 2801 GCGGAGGAC AACTCACGA CCAAGCCTCC CAGCTCTGAC TCAAGCTGAC CAGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 410 P E N N Y K T T P F V L D S D G S F F L Y S K L T V D K S R W Q Q
 2901 GCGGAGGAC AACTCACGA CCAAGCCTCC CAGCTCTGAC TCAAGCTGAC CAGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O
 3001 CTAGATGCTC TACGCTGAG GCGACGCTGAG TGGCGCGCGG GCGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 3101 TTAANTTATC AAGCGATCA GCGACGCTGAG TGGCGCGCGG GCGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 3201 TTAATGCGGT ACTGCGCGGC TGGCGCGCGG GCGCTCTGAG TGGCGCGCGG GCGCTCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC TCAAGCTGAC
 3301

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FIG._20c

*Start Tet Resistance Coding Sequence

1 GAATTCACACT TCCTCCACTT TTGGATAGGG AATACACAGC ATGAAAATAC TCATTCTCTGA GTTGTATTATT AAGCTTGGCC AAAAAGAGA AGAGTCGAAT
CTTAAGTTGA AGAGTATAGA AACCTTTGAG TTATATCTGCTA CTGCAATTTAG TGGCAATGACT CACCAATPAA TTGCAACGGG TTTCATTTCTT CAGGTAGAGTA
101 AAGCTGTGG CAGGATAGGA AGCTTTTGGG ATTAATCGTCA CTGCAATTTAG TGGCAATGACT CACCAATPAA TTGCAACGGG TTTCATTTCTT CAGGTAGAGTA
CTTGACACAC GCGTCCACTT TCGAAACCTC TAATAGCAAT GACCTTACGA AGGCTTATAC CCGCTTTTAC TGGTGTGCG CACTTAACTA GTCCATCTCC
201 GCGCGCTGTG AGAGTAAAG CGGATGCGCA GCAATCTCTGA CCGATGATGCG CAGCTACCTG CAGCTACCTG CAGCTACCTG CAGCTACCTG CAGCTACCTG
CGGCAACAT GCTCCATTTT GGGCTACGCT GTGTAGAGCT GTGTAGAGCT GTGTAGAGCT GTGTAGAGCT GTGTAGAGCT GTGTAGAGCT GTGTAGAGCT
301 AAAAGTAAAT CTTTTCALCA GCTGTCAADA AGTGTCAAG CCGGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAAAGTA TTTTGAAGTA GTACGCAAT
TTTTCAATTA GMAAAGTTGT CAGCATGATTT TACAGATGTC CCGCTCTGGA TATCAGCGAA AAAAAATTA AAAATTTACAT AAAATTTACAT CATCGCTTCA
401 TCAGTAAAC AGGTATATCA GAATTTAGAA GAAGATATAC GCATTTCTTC TTGCATCTCTA GTTCGTTTTT TCTATTGCTA CAAAGCGTA CCGTGAATTC
AGTGCATTTT TCCCATAGAT CTTATATACTT CTTCTTATAG CGTAAAGAG AGCTTAGATA CAAACAAA AATAACAGAT GTTTCGGCAT GCGCATATAG
1 *STII Signal TIR -1
M K K N I A F L L A S M F V F S I A T N A Y A D I
Anti-VesF Light chain
501 CAGTTCGACC AGTCCCGGAG CTCCTGTGTC CCGCTGTGGG GCGATAGGCT CACATFACC TGCAGCGAA CTCAGGATAT TAGCAACTAT TTAACCTGGT
GTCAACTGGG TCAGGGGCTC GAGGGACAGG CCGAGACACC CCGTATCCCA GTGTAGTGG AGCTCGGCTT CAGTCTCTATA ATCGTTGATA AAATTTGACCA
26 Q L T Q S P S A S V G D R V T I T C S A S Q D I S N Y L N W Y
601 ATCAACAGAA ACCAGARAA GTCCGAAAG TACTGATTTA CTTCACTCC TCCTCTCACT CCGGAGTCC TTTCTGCTTC TCTGATCCG GTTCTGGAGC
TAGTTGTCTT TGTGCTTTT CAGGCTTC ATGCTAAAT GAGTGGAG AGAGAGTGA GACCTCAGG AAGAGCGAG AGACTTAGG CAAAGCCCTG
60 Q Q K P G X A P K V L I Y F T S S L H S G V P S R F S G S G S G T
701 GAATTCACCT CTGACCATCA TGTGCTGCA CCACTGTCT CAGTGTGCA ACAGATPAG ACCGTCCGT GAGCTTTGG ACAAGTACC
CCTAAAGTGA GATGGTAGT COTCAGACT CCGTCTCTG AAGGTTGAA TAATGACAT TGTCTATCG TGGCAGGCA CTGCAAAAC TGTCCCATGG
93 D F T L T I S S L Q P E D F A T Y X C Q Q Y S T V P W T F G Q G T
801 AAGTGGGGA TCMAACGAC TGTGCTGCA CCACTGTCT CAGTGTGCA ACAGATPAG ACCGTCCGT GAGCTTTGG ACAAGTACC
TTCCACTCT AGTTGCTGTC ACACGAGCT GGTAGACAGA AGTAGAAGG CCGTAGACTA CTCGTCACT TTAGACTTGG AAGAGACAA CACAGCGAG
126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L
901 TGAATTAAT CTATCCAGA GAGCCAAAAG TACATGGA GGTGATPAC GCCTCTCAAT CCGGTATCT CCGAGAGAT GTCAAGCAGC AAGCAGCA
ACTTATGAA GATAGGCTT CTCGGTTTC ATGTACCTT CCACTATGG CCGGAGTTA GCCATTTAG GGTCTCTCA CAGTGTCTG TCTGTGCTT
160 N F Y P R E A K V Q W K G V D N A L Q S G N S Q E S V T E Q D S K
1001 GACACACCT TACACCTCA CACACACTT GAGCTGAGC AAGCAGAT ACAGAGACA CAAAGCTAC CCGTGGAG TCACCTCACTA GGGCTGAGC
CCTGTGCTG ATGTGCGAGT CGTGTGGA CTCGACTG GTTGTCTGTA TGTCTTTGT GTTTCAGAG CCGACCTTC AGTGGAGAT CCCGACTCG
193 D S T Y S L S T L T L S K A D Y E K H K Y A C E V T H Q G L S
1101 TCGCCGCTCA CAAAGACTT CAAAGAGGA GAGTGTAAAT TAAATCTCT ACCTGGGAC CATCTGGTAC CCGGGGATCT AGGGCTAAGG
AGCGGAGT GTTTCGAA GTTTCCTCT CTCACATTA ATTAGAGGA TGGCGGCTG GTAGCACCG TCGAGCCATG GGGCCCTAGA TCCGGATTC
226 S P V T K S F N R G E C O

FIG.-21a

1201 CTCGCTGTC GCCGGCGTT TTTATATGTT ACTCGAGCGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGAGA TTATGTCAC TGCATGCTT
 GAGCCACCG GCGCCCGCA AAAATACAA CGGCTCGCG TAGAGCTTAC TTGACACAGC CGTCATCTT CGAAATCTT AATGATCTT AATGATCTT AATGATCTT
 1301 CCGAATATG CCGCAATGAG CCGCAATGAG AGGTAGAGCG TTGATGATG AGGTAGAGCG CCGCTGTAC CCGATTAAGC CCGATCTGAC CATTCTGAC GAGGTAGAG
 CGGTATAC GCGTTTACT GTGTGTGCG AACTATGAC TCCATCTCC CCGGACATG CTCATTTCC GTGATGATG GTGATGATG GTGATGATG
 1401 ACTGCTGCG GGTATACGTA AAGATATAT TGAAGATCC TCGATGATG AAAATTAAT TTTCAACAG CCGTCAATA GTTGTATGAG CCGGATGTA
 TCGACGAGC GCTATGATCT TTCTTCAATA ACTTGTAG AGCATCATT TTTCAATAG AAAAGTGTG GACATATG CAACATGCG CCGTCTGAT
 1501 TAGTGCCTT GTTTTATTT TTTATGAT TTGTACTAG TAGCGAGTT CAGGTAAAA GGTATCTAG AATTTAGAG AAGATATG CATTCTCT
 ATCGCGAA CAAAATAA AANTATCA AACTATGAT ATGCGTTCAA GTGCATTTT CCATAGATC TTAATATCT TCTTATAG CTAAGAGA
 M K K N I A F L L
 1
 *STII Signal TIR-1
 1601 TCGATCTATG TCGTATTTT CTATGCTATC AAACGGTAC GCTGAGGTTG AGCTGTGGA GTCTGCGGT GGCCTGTGTG AGCCAGGGG CTCATCTCT
 ACGTAGATAC AAGCAAAA GATTAACATG TTTGCGCATG CGACTCCAG TGCACCACT CAGACGCCA CCGGACCAG TCGGTCCCC GAGTGAAGCA
 10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G S L R
 *Anti-VEGF Heavy Chain
 1701 TTGTCTGTG CAGCTTCTG CTACGACTC ACGACTAG GTATGAATG GTTCCGTGAG GCCCGGGA AGGCCCTGGA ATGGGTGGA TGGATTAACA
 AACAGGAC GTCGAAGAC GATGCTGAG TCGGTGATG CATCTGTAC CAGGCGATG CCGGGCCCAT TCCCGGACT TACCACACT ACCTAATGT
 43 L S C A S G Y D F T H Y G M N W V R Q A P K G L E W V G W I N T
 1801 CTTATACCG TGAACGACC TATGTCGG ATTTCAAG TCGTTTCACT TTTTCTTNG ACACCTCAA AAGCACAGCA TACTGTGAGA TGAACACT
 GGATATGCC ACTTGGCTG ATPACAGCC TAAATTTTC ACAAATGA AAAAGAAATC TGTGAGGTT TCTGTGTCT ATGACGCTCT ACTTGTGGA
 77 Y T G E P T Y A A D F K R F T F S L D T S K S T A Y L Q M N S L
 1901 GCGGCTGAG GACTGCGG TCTATTAAG TGCNAATAC CCGTACTATT ACGGACGAG CACTGTGTAT TTCAGTCTT GGGTCTGAG AACCTGCTG
 CCGCGACT CTGTGACGG AGATATGAC ACGTTTCTG GGCATGATA TGCCTGTCT GTGTACCAT AAGTGCAGA CCCAGTTC TTGGGACCA
 110 R A E D T A V Y Y C A K Y Y G T S H W Y F D V W G Q G T L V
 2001 ACGTCTCT GGCCTTCC CAAAGGCCA TCGGTCTTC CCGTGGAC CTCTCCAG AGCACTCTG GGGGACAGC GGGCTTGGC TCGTGTGTA
 TGGCAGAGA GCGGAGGTG GTTCCCGGT AGCCAGAGG GGGACCGTG GAGAGGTTC TGTGTGGA CCCGTGTG CCGGACCCG AGCGACTCA
 143 T V S S A S T K G G S V F P L A P S S K S T S G G T A A L G C L V K
 2101 AGGATACTT CCCCAGCC GTGAGGTCT CBTGACTC AGGCGCTCT ACAGCGCG TGCACACTT CCGGCTVTC CTACGATCT CAGAGCTTA
 TCTTGATGA GGGGCTTGG CACTGACCA GCACTTGA TCCCGGCA TCGTCCGC AGCTGTGGA GGGCCGACAG GATGTGAGA GTCTGATG
 177 D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y
 2201 CTCCTTCA ACGGTGTGA CTGTGCTTC TAGCACTG GCAACCGA CCACTATG CCACTGAT CAGAGCCA GGAACCAA GGTGACCA
 GAGGAGTG TGCACACT GACACGGAG CCGTGGCTT GATGTAGAG GTTGACTTA GTTGTGGT CGTGTGGT CCACCTGTC
 210 S L S S V V T V P S S L G T Q T Y I C N V N H K P S N T K V D K

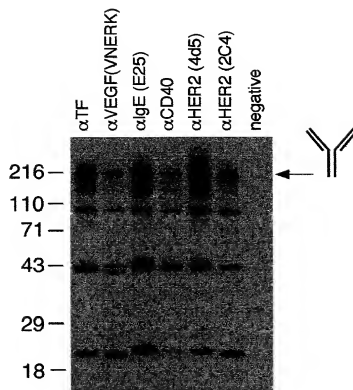
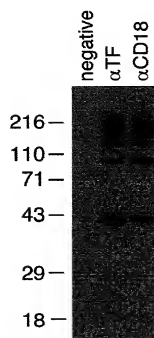
FIG..21b

2301 AAGTTGAGC CAAATCTTG TGACAAACT CACATATCC CACGTCGCC AGCACTGAA CTCCTGGGG GACGTCAGT CTTCCTCTTC CCCCACAAAC
 TTTCACCTG GATTAGACG ACTGTTTGA GTGTACGG GTGCGACGG TGTGTGACT GTGGACCCC CTGGCATCA GAAGAGAGF GGGGTTTGG
 243 K V E P K S C D K T H T C P P C P P A E L L G G P S V F L F P P K P
 2401 CAAGAGAC CCAATGATC TCCGACGCC CTGAGTCAC ATGCGTGGT GTGAGCTGA CCACAGAGA CCGTAGAGTC AAGTTCACT GTTACGTGA
 GGTTCCTGT GAGATCTAG AGGCTCATG TACGACAC CACTCTCAT CCGCTCTCT GTGACTCTAG TTCACTCTAG CCATCGACT
 277 K D T L M I S R T P E V T C V V D V S H E D P E V K F N W Y V D
 2501 GCGCTGGG GTGCATANG CCAGAGAAA GCGCGGGG GAGCAGTAC ACAGACATG CCGTGTGTC AGCTCTCTCA CGTCTCTGCA CCAGACTGG
 GCGCACCTC CACGATATAC GTTCTGTGT CCGCGCCCTC CTCTCATGT TGTCTGTGAT GGCACACAG TCGCAGAGT GGCAGAGCT GGTCTCTGAC
 310 G V E V H N A K T K P R E E Q X Y N S T Y R V V S V L T V L H Q D W
 2601 CTGAATGGA AGAGTACAA GTGCAGGTC TCCACAAAG CCTCTCCAG CCCCATGAG AAACCAATC CCAGAGCAA AGGCAAGCCC CGAGACAC
 GACTTACCT TCTCATGTT CACGTTCCAG AGGTGTTTC GCGAGGGTG GGGTAGCTC TTTTGTAGA GTTTCGTT TCCGTCGG GCTTCTGTG
 343 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q
 2701 AGGTGTAC CCTGCCCA TCCCGGGA AGATACCAA GAACAGGTC AGCTGACT GCTGTGCTA AGGCTTCTAT CCCAGGACA TCGCGTGA
 TCCACATGT GAGCGGGGT AGGCGCTTC TCTACTGTT CTGTGTCAG TCGGACTGA CGACACAGT TCCGAGATA GGTCTGCTGT AGCGCACT
 377 V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E
 2801 GTGGAGAG AATGGGAGC CTAAGAC CAGCTCCG TGTGTGACT GCGAGGCTC TTCTCTCT ACACAGT ACAGCTGAC CACGCTGAC
 CACCTCTCG TTACCGTGC GCTCTGTT GATGTCCTG TCGGAGGG ACAGCTGAG GCTGCCAGG AAGAAGAGA TGTCTGCA GTGGCACTG
 410 W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D
 2901 AAGAGCAGT GGCAGAGG GAGCTCTC TATGTCAG GCTCTGAC AACCTACA CCGAGAAG CTTCTCTCTG TCTCGGTA
 TTCTCTGCA CGTGTGCC CTTGACAG AGTACAGG ACTACGACT CCGAGAGTG TTGTGATGT GCGTCTCTC GAGAGGAC AGAGGCCAT
 443 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K
 3001 AATAAGCAT GAGAGGCCCT AGAGTCCCTA ACCTCGGT GCTTTTAT GTTAACTAT GTTTGACG TATATGCA TAAGCTTAA
 TTATGTGAC GCTGCCGGA TCTCAGGAT TCGAGCCA CCGGGGCCG CAAAATAA CAATTGATG CAACTGTCT AATGATGCT ATTGCAATT
 477 0
 3101 TCGCTAGT TATCAGTT AATTTGCTAA CGCATGACG CACCTGTAT GAATCTAAC AATGGCTCA TCGTCATCT CCGCAAGCT ACCCTGGATG
 AGCCATCAA ATAGTGTCAA TTATAGATT GCTCATGTC GTGGACATA CTTTAGATT TTACCGAGT ACAGTAGA GCGGTGGCAG TGGGACCTAC
 3201 CTGTAGGAT AGCTTGTGT ATGCCGTAC TGCGGGCT CTTCGGCAT ATGCTCAT CTGACAGT CCGCAGTAC GTGGGTGC TGTAGCGT
 GATCTCGTA TCGAACCIA TACGGCATG ACGGCCCGA GAAAGCCCTA TAGCAGTAA GCTCTGTA GCGGTGATG ATACCGCAG AGATCCGCA
 3301

*Start Tet Resistance Coding Sequence

FIG.-21c

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**FIG._22A****FIG._22B**